

Abstract

There is disclosed 103 novel methylation-altered DNA sequences ("marker sequences") that have distinct methylation patterns in cancer, compared to normal tissue. In many instances, these marker sequences represent novel sequences not found in the GenBank data base, and none of these marker sequences have previously been characterized with respect to their methylation pattern in human cancers including, but not limited to those of bladder and prostate. These 103 sequences have utility as diagnostic, prognostic and therapeutic markers in the treatment of human cancer, and as reagents in kits for detecting methylated CpG-containing nucleic acids.